

SEQUENCE LISTING

<110> Yasuhiko MUNAKATA et al.

<120> Novel human parvovirus B19 receptor and uses thereof

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<212> PRT

10 <213> Homo sapiens

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35 40 45

Glu Asn Lys Asp Glu Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr

50 55 60

20 Asp Asn Pro Leu Ser Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His

65 70 75 80

Arg His Leu Met Leu Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Ser

85 90 95

Lys Ile Gln Pro Gly Ser Gln Gln Ala Asp Phe Leu Asp Ala Leu Ile

25 100 105 110

Val Ser Met Asp Val Ile Gln His Glu Thr Ile Gly Lys Lys Phe Glu

115 120 125

Lys Arg His Ile Glu Ile Phe Thr Asp Leu Ser Ser Arg Phe Ser Lys
 130 135 140
 Ser Gln Leu Asp Ile Ile Ile His Ser Leu Lys Lys Cys Asp Ile Ser
 145 150 155 160
 5 Leu Gln Phe Phe Leu Pro Phe Ser Leu Gly Lys Glu Asp Gly Ser Gly
 165 170 175
 Asp Arg Gly Asp Gly Pro Phe Arg Leu Gly Gly His Gly Pro Ser Phe
 180 185 190
 Pro Leu Lys Gly Ile Thr Glu Gln Gln Lys Glu Gly Leu Glu Ile Val
 10 195 200 205
 Lys Met Val Met Ile Ser Leu Glu Gly Glu Asp Gly Leu Asp Glu Ile
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 Tyr Ser Phe Ser Glu Ser Leu Arg Lys Leu Cys Val Phe Lys Lys Ile
 225 230 235 240
 15 Glu Arg His Ser Ile His Trp Pro Cys Arg Leu Thr Ile Gly Ser Asn
 245 250 255
 Leu Ser Ile Arg Ile Ala Ala Tyr Lys Ser Ile Leu Gln Glu Arg Val
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 Lys Lys Thr Trp Thr Val Val Asp Ala Lys Thr Leu Lys Lys Glu Asp
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 Ile Gln Lys Glu Thr Val Tyr Cys Leu Asn Asp Asp Asp Glu Thr Glu
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 Val Leu Lys Glu Asp Ile Ile Gln Gly Phe Arg Tyr Gly Ser Asp Ile
 305 310 315 320
 25 Val Pro Phe Ser Lys Val Asp Glu Glu Gln Met Lys Tyr Lys Ser Glu
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 Gly Lys Cys Phe Ser Val Leu Gly Phe Cys Lys Ser Ser Gln Val Gln

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	Asp Asp Glu Ala Ala Ala Val Ala Leu Ser Ser Leu Ile His Ala Leu		
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	Asp Asp Leu Asp Met Val Ala Ile Val Arg Tyr Ala Tyr Asp Lys Arg		
	385	390	395
	Ala Asn Pro Gln Val Gly Val Ala Phe Pro His Ile Lys His Asn Tyr		
	405	410	415
10	Glu Cys Leu Val Tyr Val Gln Leu Pro Phe Met Glu Asp Leu Arg Gln		
	420	425	430
	Tyr Met Phe Ser Ser Leu Lys Asn Ser Lys Lys Tyr Ala Pro Thr Glu		
	435	440	445
	Ala Gln Leu Asn Ala Val Asp Ala Leu Ile Asp Ser Met Ser Leu Ala		
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	Lys Lys Asp Glu Lys Thr Asp Thr Leu Glu Asp Leu Phe Pro Thr Thr		
	465	470	475
	Lys Ile Pro Asn Pro Arg Phe Gln Arg Leu Phe Gln Cys Leu Leu His		
	485	490	495
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	500	505	510
	Trp Asn Met Leu Asn Pro Pro Ala Glu Val Thr Thr Lys Ser Gln Ile		
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	Pro Leu Ser Lys Ile Lys Thr Leu Phe Pro Leu Ile Glu Ala Lys Lys		
25	530	535	540
	Lys Asp Gln Val Thr Ala Gln Glu Ile Phe Gln Asp Asn His Glu Asp		
	545	550	555
			560

	Gly	Pro	Thr	Ala	Lys	Lys	Leu	Lys	Thr	Glu	Gln	Gly	Gly	Ala	His	Phe	
					565					570					575		
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5	Asn	Pro	Ala	Glu	Asn	Phe	Arg	Val	Leu	Val	Lys	Gln	Lys	Lys	Ala	Ser	
					595					600					605		
	Phe	Glu	Glu	Ala	Ser	Asn	Gln	Leu	Ile	Asn	His	Ile	Glu	Gln	Phe	Leu	
					610					615					620		
	Asp	Thr	Asn	Glu	Thr	Pro	Tyr	Phe	Met	Lys	Ser	Ile	Asp	Cys	Ile	Arg	
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					675					680					685		
	Glu	Glu	Ala	Ser	Gly	Ser	Ser	Val	Thr	Ala	Glu	Glu	Ala	Lys	Lys	Phe	
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	Leu	Ala	Pro	Lys	Asp	Lys	Pro	Ser	Gly	Asp	Thr	Ala	Ala	Val	Phe	Glu	
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<213> Homo sapiens

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Met Val Arg Ser Gly Asn Lys Ala Ala

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5

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gtt gtg ctg tgt atg gac gtg ggc ttt acc atg agt aac tcc att cct 102

Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser Asn Ser Ile Pro

10

15

20

25

10

ggt ata gaa tcc cca ttt gaa caa gca aag aag gtg ata acc atg ttt 150

Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val Ile Thr Met Phe

30

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40

gta cag cga cag gtg ttt gct gag aac aag gat gag att gct tta gtc 198

15

Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu Ile Ala Leu Val

45

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55

ctg ttt ggt aca gat ggc act gac aat ccc ott tct ggt ggg gat cag 246

Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser Gly Gly Asp Gln

20

60

65

70

tat cag aac atc aca gtg cac aga cat ctg atg cta cca gat ttt gat 294

Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu Pro Asp Phe Asp

75

80

85

25

ttg ctg gag gac att gaa agc aaa atc caa cca ggt tct caa cag gct 342

Leu Leu Glu Asp Ile Glu Ser Lys Ile Gln Pro Gly Ser Gln Gln Ala

	90	95	100	105	
	gac ttc ctg gat gca cta atc gtg agc atg gat gtg att caa cat gaa				390
	Asp Phe Leu Asp Ala Leu Ile Val Ser Met Asp Val Ile Gln His Glu				
5		110	115	120	
	aca ata gga aag aag ttt gag aag agg cat att gaa ata ttc act gac				438
	Thr Ile Gly Lys Lys Phe Glu Lys Arg His Ile Glu Ile Phe Thr Asp				
		125	130	135	
10	ctc agc agc cga ttc agc aaa agt cag ctg gat att ata att cat agc				486
	Leu Ser Ser Arg Phe Ser Lys Ser Gln Leu Asp Ile Ile Ile His Ser				
		140	145	150	
15	ttg aag aaa tgt gac atc tcc ctg caa ttc ttc ttg cct ttc tca ott				534
	Leu Lys Lys Cys Asp Ile Ser Leu Gln Phe Phe Leu Pro Phe Ser Leu				
		155	160	165	
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20	Gly Lys Glu Asp Gly Ser Gly Asp Arg Gly Asp Gly Pro Phe Arg Leu				
	170	175	180	185	
	ggc aag gaa gat gga agt ggg gac aga gga gat ggc ccc ttt cgc tta				630
	Gly Gly His Gly Pro Ser Phe Pro Leu Lys Gly Ile Thr Glu Gln Gln				
25		190	195	200	
	aaa gaa ggt ctt gag ata gtg aaa atg gtg atg ata tct tta gaa ggt				678

	Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu Glu Gly	
	205 210 215	
	gaa gat ggg ttg gat gaa att tat tca ttc agt gag agt ctg aga aaa	726
5	Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu Arg Lys	
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	ctg tgc gtc ttc aag aaa att gag agg cat tcc att cac tgg ccc tgc	774
	Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp Pro Cys	
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	cga ctg acc att ggc tcc aat ttg tct ata agg att gca gcc tat aaa	822
	Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala Tyr Lys	
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	tcg att cta cag gag aga gtt aaa aag act tgg aca gtt gtg gat gca	870
	Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val Asp Ala	
	270 275 280	
20	aaa acc cta aaa aaa gaa gat ata caa aaa gaa aca gtt tat tgc tta	918
	Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr Cys Leu	
	285 290 295	
	aat gat gat gat gaa act gaa gtt tta aaa gag gat att att caa ggg	966
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	Phe Arg Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp Glu Glu	
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	Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu Gly Phe	
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10	Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn Gln Val	
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	cta aag gtc ttt gca gca aga gat gat gag gca gct gca gtt gca ctt	1158
	Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Ala Val Ala Leu	
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	ttc tcc ctg att cat gct ttg gat gac tta gac atg gtg gcc ata gtt	1206
	Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala Ile Val	
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20	cga tat gct tat gac aaa aga gct aat cct caa gtc ggc gtg gct ttt	1254
	Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val Ala Phe	
	395 400 405	
25	cct cat atc aag cat aac tat gag tgt tta gtg tat gtg cag ctg cct	1302
	Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln Leu Pro	
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	Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys Asn Ser	
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5	aag aaa tat gct ccc acc gag gca cag ttg aat gct gtt gat gct ttg	1398
	Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp Ala Leu	
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10	att gac tcc atg agc ttg gca aag aaa gat gag aag aca gac acc ctt	1446
	Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp Thr Leu	
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	gaa gac ttg ttt cca acc acc aaa atc cca aat cct cga ttt cag aga	1494
15	Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe Gln Arg	
	475 480 485	
	tta ttt cag tgt ctg ctg cac aga gct tta cat ccc cgg gag cct cta	1542
	Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu Pro Leu	
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	ccc cca att cag cag cat att tgg aat atg ctg aat cct ccc gct gag	1590
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25	gtg aca aca aaa agt cag att cct ctc tct aaa ata aag acc ctt ttt	1638
	Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr Leu Phe	

	525	530	535	
	cct ctg att gaa gcc aag aaa aag gat caa gtg act gct cag gaa att	1686		
	Pro Leu Ile Glu Ala Lys Lys Lys Asp Gln Val Thr Ala Gln Glu Ile			
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	gag caa ggg gga gcc cac ttc agc gtc tcc agt ctg gct gaa ggc agt	1782		
	Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu Gly Ser			
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15	gtc acc tct gtt gga agt gtg aat cct gct gaa aac ttc cgt gtt cta	1830		
	Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg Val Leu			
	590	595	600	
	gtg aaa cag aag aag gcc agc ttt gag gaa gcg agt aac cag ctc ata	1878		
20	Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln Leu Ile			
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	Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr Phe Met			
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	Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile Lys Phe	
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	650 655 660 665	
	gtg gaa att aaa caa tta aat cat ttc tgg gaa att gtt gtc cag gat	2070
	Val Glu Ile Lys Gln Leu Asn His Phe Trp Glu Ile Val Val Gln Asp	
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	gga att act ctg atc acc aaa gag gaa gcc tot gga agt tct gtc aca	2118
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	gct gag gaa gcc aaa aag ttt ctg gcc ccc aaa gac aaa cca agt gga	2166
	Ala Glu Glu Ala Lys Lys Phe Leu Ala Pro Lys Asp Lys Pro Ser Gly	
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	715 720 725	
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25	Asp Met Ile	
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